

SEQUENCE LISTING

<110> Syrrx, Inc.
<120> CRYSTALLIZATION OF DIPEPTIDYL PEPTIDASE IV (DPPIV)
<130> SYR-DPPIV-5001-C1
<140> Not Yet Assigned
<141> 2003-09-09
<150> US 60/409,206
<151> 2002-09-09
<160> 3
<170> PatentIn version 3.1
<210> 1
<211> 766
<212> PRT
<213> Homo sapiens

<220>
<221> Amino acid sequence for full-length human wild type DPPIV
<222> (1)..(766)
<223>

<300>
<308> Genbank/NP_001926
<309> 2002-02-19
<313> (1)..(766)

<400> 1

Met Lys Thr Pro Trp Lys Val Leu Leu Gly Leu Leu Gly Ala Ala Ala
1 5 10 15

Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
65 70 75 80

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
85 90 95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
145 150 155 160

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
165 170 175

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
180 185 190

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
225 230 235 240

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
245 250 255

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
260 265 270

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
275 280 285

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr
290 295 300

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln
305 310 315 320

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg
325 330 335

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly
340 345 350

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly
355 360 365

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile
370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly
385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
420 425 430

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu
435 440 445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu
450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr
465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp
485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys
500 505 510

Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro
755 760 765

<211> 2184
<212> DNA
<213> Homo sapiens

<220>
<221> Human cDNA sequence encoding residues 39-766 of DPPIV
<222> (1)..(2184)
<223>

<400> 2

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tccttaagat ggatttcaga tcatgaatat ctctacaac aagaaaataa tatcttgta	120
ttcaatgctg aatatggaaa cagctcagtt ttcttgaga acagtagcatt tgatgagttt	180
ggacattcta tcaatgatta ttcaatatct cctgatggc agtttattct cttagaatac	240
aactacgtga agcaatggag gcattcctac acagcttcat atgacattta tgatttaat	300
aaaaggcagc tgattacaga agagaggatt ccaaacaaca cacagtgggt cacatggta	360
ccagtgggtc ataaattggc atatgttgg aacaatgaca tttatgttaa aattgaacca	420
aatttaccaa gttacagaat cacatggacg gggaaagaag atataatata taatggaata	480
actgactggg tttatgaaga ggaagtcttc agtgctact ctgctctgt gtggctcca	540
aacggcactt ttttagcata tgcccaattt aacgacacag aagtcccact tattgaatac	600
tccttctact ctgatgagtc actgcagtc ccaaagactg tacgggttcc atatccaaag	660
gcaggagctg tgaatccaac tggaaagttc tttgttgtaa atacagactc tctcagctca	720
gtcaccaatg caacttccat acaaattact gctccctgctt ctatgttcat agggatcac	780
tacttgttg atgtgacatg ggcaacacaa gaaagaattt cttgcagtg gctcaggagg	840
attcagaact attcggtcat ggatatttg gactatgtg aatccagtgg aagatggaac	900
tgcttagtgg cacggcaaca cattgaaatg agtactactg gctgggttgg aagatttagg	960
ccttcagaac ctcattttac ccttgatggt aatagttct acaagatcat cagcaatgaa	1020
gaaggttaca gacacatttgc tatttccaa atagataaaa aagactgcac atttattaca	1080
aaaggcacct gggaaagtcat cgggatagaa gctctaaccg gtgattatct atactacatt	1140
agtaatgaat ataaaggaat gccaggagga aggaatctt ataaaatcca acttattgac	1200
tatacaaaaag tgacatgcct cagttgtgag ctgaatccgg aaaggtgtca gtactattct	1260
gtgtcattca gtaaagaggc gaagtattat cagctgagat gttccgggtcc tggtctgcc	1320
ctctataactc tacacacgcg cgtgaatgtaa aagggctga gagtcctgga agacaattca	1380
gcattggata aaatgctgca gaatgtccag atgcctcca aaaaactgga cttcatttatt	1440

ttgaatgaaa caaaattttg gtatcagatg atcttcgcctc ctcattttga taaatccaag 1500
aaatatcctc tactattaga tgtgtatgca ggcccatgta gtcaaaaagc agacactgtc 1560
ttcagactga actgggccac ttaccttgca agcacagaaa acattatagt agctagctt 1620
gatggcagag gaagtggta ccaaggagat aagatcatgc atgcaatcaa cagaagactg 1680
ggaacatttg aagttgaaga tcaaattgaa gcagccagac aattttcaaa aatgggattt 1740
gtggacaaca aacgaattgc aatttgggc tggcatatg gagggtacgt aacctaattg 1800
gtcctggat cgaaaagtgg cgtgttcaag tgtggatag ccgtggcgcc tgtatcccgg 1860
tgggagtaact atgactcagt gtacacagaa cgttacatgg gtctcccaac tccagaagac 1920
aaccttgacc attacagaaa ttcaacagtc atgagcagag ctgaaaattt taaacaagtt 1980
gagtacctcc ttattcatgg aacagcagat gataacgttc actttcagca gtcagctcag 2040
atctccaaag ccctggtcga tggtagtg gattccagg caatgtggta tactgatgaa 2100
gaccatggaa tagctacgag cacagcacac caacatatat atacccacat gagccacttc 2160
ataaaaacaat gtttctcttt acct 2184

<210> 3
<211> 740
<212> PRT
<213> Homo sapiens

<220>
<221> Amino acid sequence for residues 39-766 of DPPIV
<222> (13)..(740)
<223>

<220>
<221> Amino acid sequence for residues 39-766 of DPPIV with N-terminal 6x-histidine tag
<222> (1)..(740)
<223> N-terminal 6x-histidine tag (residues 1-12)

<400> 3

Ala Asp Pro Gly Gly Ser His His His His His Ser Arg Lys Thr
1 5 10 15

Tyr Thr Leu Thr Asp Tyr Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr
20 25 30

Ser Leu Arg Trp Ile Ser Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn
35 40 45

Asn Ile Leu Val Phe Asn Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu
50 55 60

Glu Asn Ser Thr Phe Asp Glu Phe Gly His Ser Ile Asn Asp Tyr Ser
65 70 75 80

Ile Ser Pro Asp Gly Gln Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys
85 90 95

Gln Trp Arg His Ser Tyr Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn
100 105 110

Lys Arg Gln Leu Ile Thr Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp
115 120 125

Val Thr Trp Ser Pro Val Gly His Lys Leu Ala Tyr Val Trp Asn Asn
130 135 140

Asp Ile Tyr Val Lys Ile Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr
145 150 155 160

Trp Thr Gly Lys Glu Asp Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val
165 170 175

Tyr Glu Glu Glu Val Phe Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro
180 185 190

Asn Gly Thr Phe Leu Ala Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro
195 200 205

Leu Ile Glu Tyr Ser Phe Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys
210 215 220

Thr Val Arg Val Pro Tyr Pro Lys Ala Gly Ala Val Asn Pro Thr Val
225 230 235 240

Lys Phe Phe Val Val Asn Thr Asp Ser Leu Ser Ser Val Thr Asn Ala
245 250 255

Thr Ser Ile Gln Ile Thr Ala Pro Ala Ser Met Leu Ile Gly Asp His
260 265 270

Tyr Leu Cys Asp Val Thr Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln
 275 280 285

Trp Leu Arg Arg Ile Gln Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr
290 295 300

Asp Glu Ser Ser Gly Arg Trp Asn Cys Leu Val Ala Arg Gln His Ile
305 310 315 320

Glu Met Ser Thr Thr Gly Trp Val Gly Arg Phe Arg Pro Ser Glu Pro
 325 330 335

His Phe Thr Leu Asp Gly Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu
 340 345 350

Glu Gly Tyr Arg His Ile Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys
 355 360 365

Thr Phe Ile Thr Lys Gly Thr Trp Glu Val Ile Gly Ile Glu Ala Leu
 370 375 380

Thr Ser Asp Tyr Leu Tyr Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro
 385 390 395 400

Gly Gly Arg Asn Leu Tyr Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val
 405 410 415

Thr Cys Leu Ser Cys Glu Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser
 420 425 430

Val Ser Phe Ser Lys Glu Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly
435 440 445

Pro Gly Leu Pro Leu Tyr Thr Leu His Ser Ser Val Asn Asp Lys Gly
450 455 460

Leu Arg Val Leu Glu Asp Asn Ser Ala Leu Asp Lys Met Leu Gln Asn
165 170 175 180

Val Gln Met Pro Ser Lys Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr
185 186 187 188 189

Lys Phe Trp Tyr Gln Met Ile Leu Pro Pro His Phe Asp Lys Ser Lys
500 505 510

Lys Tyr Pro Leu Leu Leu Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys
515 520 525

Ala Asp Thr Val Phe Arg Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr
530 535 540

Glu Asn Ile Ile Val Ala Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln
545 550 555 560

Gly Asp Lys Ile Met His Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu
565 570 575

Val Glu Asp Gln Ile Glu Ala Ala Arg Gln Phe Ser Lys Met Gly Phe
580 585 590

Val Asp Asn Lys Arg Ile Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr
595 600 605

Val Thr Ser Met Val Leu Gly Ser Gly Ser Gly Val Phe Lys Cys Gly
610 615 620

Ile Ala Val Ala Pro Val Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr
625 630 635 640

Thr Glu Arg Tyr Met Gly Leu Pro Thr Pro Glu Asp Asn Leu Asp His
645 650 655

Tyr Arg Asn Ser Thr Val Met Ser Arg Ala Glu Asn Phe Lys Gln Val
660 665 670

Glu Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn Val His Phe Gln
675 680 685

Gln Ser Ala Gln Ile Ser Lys Ala Leu Val Asp Val Gly Val Asp Phe
690 695 700

Gln Ala Met Trp Tyr Thr Asp Glu Asp His Gly Ile Ala Ser Ser Thr
705 710 715 720

Ala His Gln His Ile Tyr Thr His Met Ser His Phe Ile Lys Gln Cys

725

730

735

Phe Ser Leu Pro
740